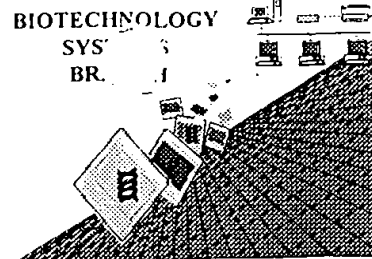


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/806,232

Source: PCT09

Date Processed by STIC: 4-4-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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PCT
09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001

TIME: 11:23:01

Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

3 <110> APPLICANT: Seiki Motoharu
 5 <120> TITLE OF INVENTION: DNA CODING FOR NOVEL POLIPEPTIDE
 W--> 7 <130> FILE REFERENCE:
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/806,232
 C--> 10 <141> CURRENT FILING DATE: 2001-03-28
 12 <150> PRIOR APPLICATION NUMBER: JP10-276258
 13 <151> PRIOR FILING DATE: 1998-09-29
 15 <150> PRIOR APPLICATION NUMBER: JP10-291505
 16 <151> PRIOR FILING DATE: 1998-09-29
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
 Corrected Diskette Needed
 see pp. 1-8

ERRORED SEQUENCES

259 <210> SEQ ID NO: 3
 260 <211> LENGTH: 3517
 E--> 261 <212> TYPE: *Missing mandatory sequence type*
 262 <213> ORGANISM: Mouse *DNA, RNA, PRT*
 264 <220> FEATURE:
 265 <221> NAME/KEY: CDS
 266 <222> LOCATION: (86)..(1846)
 268 <400> SEQUENCE: 3
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 271 tcgccaccgc acctgggaga gcggg atg gga cgc cgc cgg gga cct ggg 112
 272 Met Gly Arg Arg Pro Arg Gly Pro Gly
 273 1 5
 275 tcc ccc cgg gga cct ggc cct cca cgc ccc ggg ccg ggg ctg cca cca 160
 276 Ser Pro Arg Gly Pro Gly Pro Pro Arg Pro Gly Pro Gly Leu Pro Pro
 277 10 15 20 25
 279 ctg ctg ctt gta ctg gcg ctg gcg gcc cat ggg ggc tgc gca gcg ccc 208
 280 Leu Leu Leu Val Leu Ala Leu Ala Ala His Gly Gly Cys Ala Ala Pro
 281 30 35 40
 283 gcg ccc cgc gcg gag gac ctc agc ctc ggg gtg gag tgg cta agc agg 256
 284 Ala Pro Arg Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg
 285 45 50 55
 287 ttt ggc tac ctg ccg cct gca gat ccg gca tca ggg cag cta cag acc 304
 288 Phe Gly Tyr Leu Pro Pro Ala Asp Pro Ala Ser Gly Gln Leu Gln Thr
 289 60 65 70
 291 cag gag gaa ctg tcc aaa gcg att act gcc atg cag cag ttt ggt ggt 352
 292 Gln Glu Glu Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly
 293 75 80 85
 295 ctg gag acc act ggc atc cta gat gag gcc act ctg gcc ctg atg aaa 400
 296 Leu Glu Thr Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys
 297 90 95 100 105
 299 acc cct cga tgc tcc ctt ccg gac ctg ccc cct ggg gcc caa tcg aga 448
 300 Thr Pro Arg Cys Ser Leu Pro Asp Leu Pro Pro Gly Ala Gln Ser Arg

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Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

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303	agg aag cgg cag act cca ccc cca acc aaa tgg agc aag agg aac ctt	496						
304	Arg Lys Arg Gln Thr Pro Pro Pro Thr Lys Trp Ser Lys Arg Asn Leu							
305		125		130		135		
307	tct tgg agg gtc cgg aca ttc cca cgg gac tca ccc ctg ggc cgg gat	544						
308	Ser Trp Arg Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly Arg Asp							
309		140		145		150		
311	act gtg cgt gca ctc atg tac tac gcc ctc aaa gtc tgg agt gac atc	592						
312	Thr Val Arg Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile							
313		155		160		165		
315	aca ccc ttg aac ttc cac gag gta gcg ggc aac gcg gcg gac atc cag	640						
316	Thr Pro Leu Asn Phe His Glu Val Ala Gly Asn Ala Ala Asp Ile Gln							
317	170		175		180		185	
319	atc gac ttc tcc aag gcc gac cac aat gac ggc tac ccc ttc gat ggc	688						
320	Ile Asp Phe Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly							
321		190		195		200		
323	cct ggt ggc acg gtg gcc cac gca ttc ttc cct ggt gac cac cac acg	736						
324	Pro Gly Gly Thr Val Ala His Ala Phe Phe Pro Gly Asp His His Thr							
325		205		210		215		
327	gca ggg gac acc cac ttt gat gac gat gag cca tgg acc ttc cgt tcc	784						
328	Ala Gly Asp Thr His Phe Asp Asp Asp Glu Pro Trp Thr Phe Arg Ser							
329		220		225		230		
331	tca gat gcc cac ggg atg gac ctg ttt gca gtg gcc gtc cat gag ttt	832						
332	Ser Asp Ala His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe							
333		235		240		245		
335	ggt cat gcc att ggt ctg agc cat gtt gcc gcc cca agc tcc atc atg	880						
336	Gly His Ala Ile Gly Leu Ser His Val Ala Ala Pro Ser Ser Ile Met							
337	250		255		260		265	
339	caa ccg tac tac cag ggc ccc gtg ggt gac ccc gta cgc tat gga ctt	928						
340	Gln Pro Tyr Tyr Gln Gly Pro Val Gly Asp Pro Val Arg Tyr Gly Leu							
341		270		275		280		
343	ccc tat gag gac agg gtg cgt gtc tgg cag ttg tac ggt gtg cgg gaa	976						
344	Pro Tyr Glu Asp Arg Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu							
345		285		290		295		
347	tcc gtg tcc cct act gcc cag ctg gat acc cca gag ccc gag gag cca	1024						
348	Ser Val Ser Pro Thr Ala Gln Leu Asp Thr Pro Glu Pro Glu Glu Pro							
349		300		305		310		
351	ccc ctc ctg cca gag ccc ccc aac aat cgg tct agc act ccg ccc cag	1072						
352	Pro Leu Leu Pro Glu Pro Pro Asn Asn Arg Ser Ser Thr Pro Pro Gln							
353		315		320		325		
355	aag gac gtg cct cac agg tgc act gcc cac ttt gat gct gtg gcc cag	1120						
356	Lys Asp Val Pro His Arg Cys Thr Ala His Phe Asp Ala Val Ala Gln							
357	330		335		340		345	
359	att cga ggc gaa gca ttc ttt ttc aaa ggc aag tat ttc tgg agg ctg	1168						
360	Ile Arg Gly Glu Ala Phe Phe Phe Lys Gly Lys Tyr Phe Trp Arg Leu							
361		350		355		360		
363	acc cgg gac cga cac ttg gtg tgg ctg cag ccg gct caa atg cat cgc	1216						
364	Thr Arg Asp Arg His Leu Val Ser Leu Gln Pro Ala Gln Met His Arg							
365		365		370		375		

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367 ttc tgg cgg ggc ctg ccg ctg cac ctg gac agt gtg gac gcc gtg tat 1264
368 Phe Trp Arg Gly Leu Pro Leu His Leu Asp Ser Val Asp Ala Val Tyr
369          380          385          390
371 gag cgt acc agt gac cac aag att gtc ttc ttc aaa gga gac aga tac 1312
372 Glu Arg Thr Ser Asp His Lys Ile Val Phe Phe Lys Gly Asp Arg Tyr
373          395          400          405
375 tgg gtg ttt aag gac aac aac gta gag gaa ggg tac ccg cga cct gtc 1360
376 Trp Val Phe Lys Asp Asn Asn Val Glu Glu Gly Tyr Pro Arg Pro Val
377 410          415          420          425
379 tcc gac ttc agc ctc ccg cca ggt ggc atc gat gct gtc ttc tcc tgg 1408
380 Ser Asp Phe Ser Leu Pro Pro Gly Gly Ile Asp Ala Val Phe Ser Trp
381          430          435          440
383 gcc cac aat gac agg act tat ttc ttt aag gac cag ctg tac tgg cgc 1456
384 Ala His Asn Asp Arg Thr Tyr Phe Phe Lys Asp Gln Leu Tyr Trp Arg
385          445          450          455
387 tat gat gac cac aca cgg cgc atg gac cct ggc tac cct gcc cag gga 1504
388 Tyr Asp Asp His Thr Arg Arg Met Asp Pro Gly Tyr Pro Ala Gln Gly
389          460          465          470
391 ccc ctg tgg aga ggt gtc ccc agc atg ttg gat gat gcc atg cgc tgg 1552
392 Pro Leu Trp Arg Gly Val Pro Ser Met Leu Asp Asp Ala Met Arg Trp
393          475          480          485
395 tct gat ggt gca tcc tat ttc ttc cga ggc cag gag tac tgg aaa gtg 1600
396 Ser Asp Gly Ala Ser Tyr Phe Phe Arg Gly Gln Glu Tyr Trp Lys Val
397 490          495          500          505
399 ctg gat ggc gag ctg gaa gca gcc ccc ggg tac cca cag tct aca gcc 1648
400 Leu Asp Gly Glu Leu Glu Ala Ala Pro Gly Tyr Pro Gln Ser Thr Ala
401          510          515          520
403 cgc gac tgg ctg gta tgc ggt gag ccg ctg gcg gat gcg gag gat gta 1696
404 Arg Asp Trp Leu Val Cys Gly Glu Pro Leu Ala Asp Ala Glu Asp Val
405          525          530          535
407 ggg cct gga ccc cag ggc cgc agt ggg gcc caa gat ggt ctg gca gta 1744
408 Gly Pro Gly Pro Gln Gly Arg Ser Gly Ala Gln Asp Gly Leu Ala Val
409          540          545          550
411 tgt tcc tgc act tca gac gca cac agg ttg gca ctg cca tct ctg ctg 1792
412 Cys Ser Cys Thr Ser Asp Ala His Arg Leu Ala Leu Pro Ser Leu Leu
413          555          560          565
415 ctt ctg act cca ctg ctg tgg ggc ctg tgg acc tca gtc tct gcc aag 1840
416 Leu Leu Thr Pro Leu Leu Trp Gly Leu Trp Thr Ser Val Ser Ala Lys
417 570          575          580          585
419 gca tcc tgagggcagt gctagccttg cggatcaagg agccagggga gcagggacac 1896
420 Ala Ser
422 actggccagt actcagcagg acttgtgtctc caagcttccg gtcctctgct ctttcttcc 1956
424 ttcttctctt gaaccaggg gtgctgtgcc atctgtctgga gtggtctcca gctgggacag 2016
426 gacgtccac caagggcatc catgcacacc ttgctacct ggagcagcca taggcagctc 2076
428 ccttccctc ctctgcacat cacgtgtctt cgttgacact tgccgggctg cccaagccca 2136
430 gctgtcaciaa cccaggatg ccttgtctgc acctgagcgg ctctgatggc atctgcacgt 2196
432 gggctgatga ggggcaaaca ggggttccctc gtggtatccg taggggccac catgcctgtt 2256
434 tcacaagtaa gagagttgat gccccgatgg gggaacaggg tgggagaaag gcacctacc 2316
436 agaagtctga tccactgccg ttgacagcag ccagcgccgt atctgctggg ataggggacc 2376

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001

TIME: 11:23:02

Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

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440 accaggagca cagccacctc tccccgtcct agataggtta gccatggagg ctgtgtcctg 2496
442 ttatctccct ctctttggcc aggagagcat tgtgggtctc cctcgggtgc tgttgatggg 2556
444 ggtggggggc gcccatagag atattttctc atctgtcagt acccattgct tcagcaagat 2616
446 gcccccatat agttctggcc tgagaccctg cagcttggac tcacagctgt cccctcccca 2676
448 gctgcagaag ggcttctaac acctggaata aaggtgggag ttcagtttag ggaaggaggga 2736
450 tgggtggggg agcccagggt gatagcaagg gggagctgca gggataagtg tcagggtcct 2796
452 cggggagtca tgacaatgtt accgcctaac ttggagatgt aggagctgtg cacggattgc 2856
454 ttctctgggt gacaaacctc catggtccag aaaggggctg aggttgaacc caagatgggt 2916
456 taatgagctc cagaaaggaa cagccaagtt caaagggttct gggacaagac gggcctgagg 2976
458 aacagggccca cccaggtagg cgtggctgta gggtaagcag tttctgtcat tgggcacgag 3036
460 atgaaaatta gtgatcacac gcacataccc cctcccccac ctggcccggg cccatctcag 3096
462 gtaagaaagg cttctgtcta ccccaggcca ggtttgagtg ttgtcaggat gagttagcag 3156
464 ctacgggggc ctaagtttct accctccatt tcccaagcct ggccacaccc tagaccctg 3216
466 tcagactagg caggacagag tcaggggtag gggcatctga ggtttccctg tcttgggaagc 3276
468 caccctactc tgccctcata tcaaagcacg ctccatgatg gtcccatgtt gtccaccagc 3336
470 ctgcaggaca cagatgtcct atacagcaac agggaaagtc caaaaatctt tgtcacatag 3396
472 cactgaaaac cagaccgcga ggctggagct gtctagatgc tgggtgtcaca ctcatTTTaa 3456
474 aacccaact cttaataaaa attttgtaca ctggaaaaaa aaaaaaaaaa aaaaaaaaaa 3516
476 a 3517

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478 <210> SEQ ID NO: 4

479 <211> LENGTH: 2423 2438

E--> 480 <212> TYPE: *Missing mandatory sequence type*

481 <213> ORGANISM: Homo sapiens

483 <220> FEATURE:

484 <221> NAME/KEY: CDS

485 <222> LOCATION: (100)..(1917)

487 <400> SEQUENCE: 4

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490 cgggaccctg cacgcgcgcc gcgggcccat gtgagcgcc atg cgg cgc cgc gca 114
491 Met Arg Arg Arg Ala
492 1
493 5
495 gcc cgg gga ccc ggc ccg ccg ccc cca ggg ccc gga ctc tcg cgg ctg 162
496 Ala Arg Gly Pro Gly Pro Pro Pro Pro Gly Leu Ser Arg Leu
497 10 15 20
499 ccg ctg ctg ccg ctg ccg ctg ctg ctg ctg gcg ctg ggg acc cgc 210
500 Pro Leu Leu Pro Leu Pro Leu Leu Leu Leu Ala Leu Gly Thr Arg
501 25 30 35
503 ggg ggc tgc gcc gcg ccg gaa ccc gcg cgg cgc gcc gag gac ctc agc 258
504 Gly Gly Cys Ala Ala Pro Glu Pro Ala Arg Arg Ala Glu Asp Leu Ser
505 40 45 50
507 ctg gga gtg gag tgg cta agc agg ttc ggt tac ctg ccc ccg gct gac 306
508 Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr Leu Pro Pro Ala Asp
509 55 60 65
511 ccc aca aca ggg cag ctg cag acg caa gag gag ctg tct aag gcc atc 354
512 Pro Thr Thr Gly Gln Leu Gln Thr Gln Glu Glu Leu Ser Lys Ala Ile
513 70 75 80 85
515 aca gcc atg cag cag ttt ggt ggc ctg gag gcc acc ggc atc ctg gac 402

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520	Glu	Ala	Thr	Leu	Ala	Leu	Met	Lys	Thr	Pro	Arg	Cys	Ser	Leu	Pro	Asp	
521				105					110					115			
523	ctc	cct	gtc	ctg	acc	cag	gct	cgc	agg	aga	cgc	cag	gct	cca	gcc	ccc	498
524	Leu	Pro	Val	Leu	Thr	Gln	Ala	Arg	Arg	Arg	Arg	Gln	Ala	Pro	Ala	Pro	
525				120					125					130			
527	acc	aag	tgg	aac	aag	agg	aac	ctg	tcg	tgg	agg	gtc	cgg	acg	ttc	cca	546
528	Thr	Lys	Trp	Asn	Lys	Arg	Asn	Leu	Ser	Trp	Arg	Val	Arg	Thr	Phe	Pro	
529				135				140					145				
531	cgg	gac	tca	cca	ctg	ggg	cac	gac	acg	gtg	cgt	gca	ctc	atg	tac	tac	594
532	Arg	Asp	Ser	Pro	Leu	Gly	His	Asp	Thr	Val	Arg	Ala	Leu	Met	Tyr	Tyr	
533	150					155					160					165	
535	gcc	ctc	aag	gtc	tgg	agc	gac	att	gcg	ccc	ctg	aac	ttc	cac	gag	gtg	642
536	Ala	Leu	Lys	Val	Trp	Ser	Asp	Ile	Ala	Pro	Leu	Asn	Phe	His	Glu	Val	
537				170						175					180		
539	gcg	ggc	agc	acc	gcc	gac	atc	cag	atc	gac	ttc	tcc	aag	gcc	gac	cat	690
540	Ala	Gly	Ser	Thr	Ala	Asp	Ile	Gln	Ile	Asp	Phe	Ser	Lys	Ala	Asp	His	
541				185					190					195			
543	aac	gac	ggc	tac	ccc	ttc	gac	ggc	ccc	ggc	ggc	acc	gtg	gcc	cac	gcc	738
544	Asn	Asp	Gly	Tyr	Pro	Phe	Asp	Gly	Pro	Gly	Gly	Thr	Val	Ala	His	Ala	
545				200					205					210			
547	ttc	ttc	ccc	ggc	cac	cac	cac	acc	gcc	ggg	gac	acc	cac	ttt	gac	gat	786
548	Phe	Phe	Pro	Gly	His	His	His	Thr	Ala	Gly	Asp	Thr	His	Phe	Asp	Asp	
549				215					220				225				
551	gac	gag	gcc	tgg	acc	ttc	cgc	tcc	tcg	gat	gcc	cac	ggg	atg	gac	ctg	834
552	Asp	Glu	Ala	Trp	Thr	Phe	Arg	Ser	Ser	Asp	Ala	His	Gly	Met	Asp	Leu	
553	230					235					240				245		
555	ttt	gca	gtg	gct	gtc	cac	gag	ttt	ggc	cac	gcc	att	ggg	tta	agc	cat	882
556	Phe	Ala	Val	Ala	Val	His	Glu	Phe	Gly	His	Ala	Ile	Gly	Leu	Ser	His	
557				250						255					260		
559	gtg	gcc	gct	gca	cac	tcc	atc	atg	cgg	ccg	tac	tac	cag	ggc	ccg	gtg	930
560	Val	Ala	Ala	Ala	His	Ser	Ile	Met	Arg	Pro	Tyr	Tyr	Gln	Gly	Pro	Val	
561				265					270					275			
563	ggt	gac	ccg	ctg	cgc	tac	ggg	ctc	ccc	tac	gag	gac	aag	gtg	cgc	gtc	978
564	Gly	Asp	Pro	Leu	Arg	Tyr	Gly	Leu	Pro	Tyr	Glu	Asp	Lys	Val	Arg	Val	
565				280					285					290			
567	tgg	cag	ctg	tac	ggt	gtg	cgg	gag	tct	gtg	tct	ccc	acg	gcg	cag	ccc	1026
568	Trp	Gln	Leu	Tyr	Gly	Val	Arg	Glu	Ser	Val	Ser	Pro	Thr	Ala	Gln	Pro	
569				295					300				305				
571	gag	gag	cct	ccc	ctg	ctg	ccg	gag	ccc	cca	gac	aac	cgg	tcc	agc	gcc	1074
572	Glu	Glu	Pro	Pro	Leu	Leu	Pro	Glu	Pro	Pro	Asp	Asn	Arg	Ser	Ser	Ala	
573	310					315					320					325	
575	ccg	ccc	agg	aag	gac	gtg	ccc	cac	aga	tgc	agc	act	cac	ttt	gac	gcg	1122
576	Pro	Pro	Arg	Lys	Asp	Val	Pro	His	Arg	Cys	Ser	Thr	His	Phe	Asp	Ala	
577				330						335					340		
579	gtg	gcc	cag	atc	cgg	ggt	gaa	gct	ttc	ttc	ttc	aaa	ggc	aag	tac	ttc	1170
580	Val	Ala	Gln	Ile	Arg	Gly	Glu	Ala	Phe	Phe	Phe	Lys	Gly	Lys	Tyr	Phe	

RAW SEQUENCE LISTING

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DATE: 04/04/2001

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Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

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581          345          350          355
583 tgg cgg ctg acg cgg gac cgg cac ctg gtg tcc ctg cag ccg gca cag 1218
584 Trp Arg Leu Thr Arg Asp Arg His Leu Val Ser Leu Gln Pro Ala Gln
585          360          365          370
587 atg cac cgc ttc tgg cgg ggc ctg ccg ctg cac ctg gac agc gtg gac 1266
588 Met His Arg Phe Trp Arg Gly Leu Pro Leu His Leu Asp Ser Val Asp
589          375          380          385
591 gcc gtg tac gag cgc acc agc gac cac aag atc gtc ttc ttt aaa gga 1314
592 Ala Val Tyr Glu Arg Thr Ser Asp His Lys Ile Val Phe Phe Lys Gly
593 390          395          400          405
595 gac agg tac tgg gtg ttc aag gac aat aac gta gag gaa gga tac ccg 1362
596 Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn Val Glu Glu Gly Tyr Pro
597          410          415          420
599 cgc ccc gtc tcc gac ttc agc ctc ccg cct ggc ggc atc gac gct gcc 1410
600 Arg Pro Val Ser Asp Phe Ser Leu Pro Pro Gly Gly Ile Asp Ala Ala
601          425          430          435
603 ttc tcc tgg gcc cac aat gac agg act tat ttc ttt aag gac cag ctg 1458
604 Phe Ser Trp Ala His Asn Asp Arg Thr Tyr Phe Phe Lys Asp Gln Leu
605          440          445          450
607 tac tgg cgc tac gat gac cac acg agg cac atg gac ccc ggc tac ccc 1506
608 Tyr Trp Arg Tyr Asp Asp His Thr Arg His Met Asp Pro Gly Tyr Pro
609          455          460          465
611 gcc cag agc ccc ctg tgg agg ggt gtc ccc agc acg ctg gac gac gcc 1554
612 Ala Gln Ser Pro Leu Trp Arg Gly Val Pro Ser Thr Leu Asp Asp Ala
613 470          475          480          485
615 atg cgc tgg tcc gac ggt gcc tcc tac ttc ttc cgt ggc cag gag tac 1602
616 Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe Phe Arg Gly Gln Glu Tyr
617          490          495          500
619 tgg aaa gtg ctg gat ggc gag ctg gag gtg gca ccc ggg tac cca cag 1650
620 Trp Lys Val Leu Asp Gly Glu Leu Glu Val Ala Pro Gly Tyr Pro Gln
621          505          510          515
623 tcc acg gcc cgg gac tgg ctg gtg tgt gga gac tca cag gcc gat gga 1698
624 Ser Thr Ala Arg Asp Trp Leu Val Cys Gly Asp Ser Gln Ala Asp Gly
625          520          525          530
627 tct gtg gct gcg ggc gtg gac gcg gca gag ggg ccc cgc gcc cct cca 1746
628 Ser Val Ala Ala Gly Val Asp Ala Ala Glu Gly Pro Arg Ala Pro Pro
629          535          540          545
631 gga caa cat gac cag agc cgc tcg gag gac ggt tac gag gtc tgc tca 1794
632 Gly Gln His Asp Gln Ser Arg Ser Glu Asp Gly Tyr Glu Val Cys Ser
633 550          555          560          565
635 tgc acc tct ggg gca tcc tct ccc ccg ggg gcc cca ggc cca ctg gtg 1842
636 Cys Thr Ser Gly Ala Ser Ser Pro Pro Gly Ala Pro Gly Pro Leu Val
637          570          575          580
639 gct gcc acc atg ctg ctg ctg ctg ccg cca ctg tca cca ggc gcc ctg 1890
640 Ala Ala Thr Met Leu Leu Leu Leu Pro Pro Leu Ser Pro Gly Ala Leu
641          585          590          595
643 tgg aca gcg gcc cag gcc ctg acg cta tgacacacag cgcgagccca 1937
644 Trp Thr Ala Ala Gln Ala Leu Thr Leu
645          600          605

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001

TIME: 11:23:02

Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

647 tgagaggaca gaggcggtgg gacagcctgg ccacagaggg caaggactgt gccggagtcc 1997
 649 ctgggggagg tgctggcgcg ggatgaggac gggccaccct ggcaccggaa ggccagcaga 2057
 651 gggcacggcc cgccagggtc gggcaggctc aggtggcaag gacggagctg tcccctagt 2117
 653 agggactgtg ttgactgacg agccgagggg tggccgctcc agaagggtgc ccagtcaggc 2177
 655 cgcaccgccg ccagcctcct ccggccctgg agggagcatc tcgggctggg ggcccccccc 2237
 657 tctctgtgcc ggcgccacca accccaccca cactgctgcc tgggtgctcc gccggcccac 2297
 659 agggcctccg tcccaggtc ccagtgagg cagccctccc cacagacgag cccccacat 2357
 661 ggtgccgcgg cagtcctccc ctgtgacgcg ttccagacca acatgacctc tcctgtctt 2417
 663 gtaaaaaaaaa aaaaaaaaaa a 2438

1360 <210> SEQ ID NO: 9

1361 <211> LENGTH: 21

E--> 1362 <212> TYPE:

1363 <213> ORGANISM: Homo sapiens

1365 <400> SEQUENCE: 9

1366 GGTTCCTCTT GTTCCACTTG G

21

1368 <210> SEQ ID NO: 10

1369 <211> LENGTH: 35

E--> 1370 <212> TYPE:

1371 <213> ORGANISM: Homo sapiens

1373 <400> SEQUENCE: 10

1374 gtaggaattc ggggtgtagg gaggtcgaca ttgcc

35

1376 <210> SEQ ID NO: 11

1377 <211> LENGTH: 23

E--> 1378 <212> TYPE:

1379 <213> ORGANISM: Homo sapiens

1381 <400> SEQUENCE: 11

1382 ggcaatgtcg acctccctac aac

1384 <210> SEQ ID NO: 12

1385 <211> LENGTH: 22

E--> 1386 <212> TYPE:

1387 <213> ORGANISM: Homo sapiens

1389 <400> SEQUENCE: 12

1390 ggagctgtct aaggccatca ca

22

1392 <210> SEQ ID NO: 13

1393 <211> LENGTH: 23

E--> 1394 <212> TYPE:

1395 <213> ORGANISM: Homo sapiens

1397 <400> SEQUENCE: 13

1398 ctccctacaa cccgaattcc tac

23

1400 <210> SEQ ID NO: 14

1401 <211> LENGTH: 20

E--> 1402 <212> TYPE:

1403 <213> ORGANISM: Homo sapiens

1405 <400> SEQUENCE: 14

1406 cttgtgggca gatagggggc

20

1408 <210> SEQ ID NO: 15

1409 <211> LENGTH: 21

E--> 1410 <212> TYPE:

1411 <213> ORGANISM: Homo sapiens

All missing mandatory
 sequence type.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001

TIME: 11:23:02

Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

1413 <400> SEQUENCE: 15
1414 cgcgccgagg acctcagcct g 21
1416 <210> SEQ ID NO: 16
1417 <211> LENGTH: 21
E--> 1418 <212> TYPE:
1419 <213> ORGANISM: Homo sapiens
1421 <400> SEQUENCE: 16
1422 ggttcctctt gttccacttg g 21
1656 <210> SEQ ID NO: 19
1657 <211> LENGTH: 21
E--> 1658 <212> TYPE:
1659 <213> ORGANISM: Homo sapiens
1661 <400> SEQUENCE: 19
1662 aatctcccat cggccctttc a 21
1664 <210> SEQ ID NO: 20
1665 <211> LENGTH: 20
E--> 1666 <212> TYPE:
1667 <213> ORGANISM: Homo sapiens
1669 <400> SEQUENCE: 20
1670 atgcacggcc accaggaaga 20
1672 <210> SEQ ID NO: 21
1673 <211> LENGTH: 20
E--> 1674 <212> TYPE:
1675 <213> ORGANISM: Homo sapiens
1677 <400> SEQUENCE: 21
1678 ggatcagaca acgatcgagt 20
1680 <210> SEQ ID NO: 22
1681 <211> LENGTH: 20
E--> 1682 <212> TYPE:
1683 <213> ORGANISM: Homo sapiens
1685 <400> SEQUENCE: 22
1686 cagcttgaag ttgtgcgtct 20

*All missing mandatory
sequence type.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001

TIME: 11:23:03

Input Set : A:\1241.18 Seq List.txt

Output Set: N:\CRF3\04042001\I806232.raw

L:7 M:201 W: Mandatory field data missing, FILE REFERENCE
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:261 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:480 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1362 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1370 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1378 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1386 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1394 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1402 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1410 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1418 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1658 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1666 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1674 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1682 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: